AMENDMENT

IN THE CLAIMS:

1. (Currently amended) A method of identifying a cancer by tumor type in a human or animal, the method comprising the steps of:

a) extracting extracellular DNA from blood plasma or serum obtained from a human or animal, wherein the extracted extracellular DNA comprises DNA species from a plurality of the human's or animal's genes, wherein at least one of said DNA species is a non-mutated tumor-associated DNA species;

b) amplifying or signal amplifying DNA from two or more genes from a portion of the extracted extracellular DNA, wherein said genes are associated with cancer and wherein at least one of said genes is a non-mutated tumor-associated gene and wherein the extracted extracellular DNA is amplified qualitatively or quantitatively, sequentially or concurrently, to produce an amplified DNA fragment or amplified signal from each of the two or more genes comprising the portion of extracellular extracted DNA; and

c) detecting the amplified DNA fragments or amplified signals from said two or more genes, wherein detection of the genes identifies the cancer by tumor type.

2. (Original) The method of claim 1, wherein the cancer tumor type is colorectal cancer, lung cancer, breast cancer, lymphoma, pancreatic cancer, bladder cancer, ovarian cancer, esophageal cancer, hepatocellular cancer, cervical cancer, melanoma, sarcoma, or leukemia.

3. (Original) The method of claim 1, wherein the genes amplified or signal amplified in step (b) are genes specific for cancer of a specific tumor type.

4. (Original) A method according to claim 3 further comprising the step of assessing a human or animal for having cancer of a particular tumor type, wherein said specific cancer tumor type is colorectal cancer, lung cancer, breast cancer, lymphoma, pancreatic cancer, bladder

cancer, ovarian cancer, esophageal cancer, hepatocellular cancer, cervical cancer, melanoma, sarcoma, or leukemia, and wherein the human or animal is determined to have a cancer of a particular tumor type when amplified DNA fragments or amplified signals of genes specific for cancer of said tumor type are detected.

5. (Cancelled)

6. (Cancelled)

7. (Cancelled)

8. (Cancelled)

9. (Cancelled)

10. (Currently amended) A method of determining a phenotype or genotype of a neoplastic tissue in a human or animal, the method comprising the steps of:

a) extracting extracellular DNA from blood plasma or serum obtained from a human or animal, wherein the extracted extracellular DNA comprises DNA species from a plurality of the human's or animal's genes, wherein at least one of said DNA species is a non-mutated tumor-associated DNA species;

b) amplifying or signal amplifying DNA from two or more genes from a portion of the extracted extracellular DNA, wherein said genes are associated with neoplastic tissue, wherein at least one of said genes is a non-mutated tumor-associated gene, and wherein the extracted extracellular DNA is amplified qualitatively or quantitatively, sequentially or concurrently, to produce an amplified DNA fragment or amplified signal from each of the two or more genes comprising the portion of extracellular extracted DNA; and

c) detecting the amplified DNA fragments or amplified signals from said two or

more genes, wherein detection of the genes identifies the neoplastic tissue and determines the phenotype or genotype thereof.

11. (Currently amended) The method of claim 10, wherein the amplified DNA in part (b) comprises at least one non-mutated, wild-type DNA species.

12. (Original) The method of claim 10, wherein the phenotype or genotype determines invasiveness of malignant cells of the neoplastic tissue.

13. (Original) The method of claim 10, wherein the phenotype or genotype determines sensitivity or resistance of the neoplastic tissue to a therapy.

14. (Original) The method of claim 10, wherein the phenotype or genotype discriminates cancer from premalignant cells or tissue.

15. (Original) The method of claim 10, wherein the phenotype or genotype is used to select the human or animal for a particular therapeutic regimen or group of regimens.

16. (Currently amended) A method for identifying a propensity in a human or animal to have or develop cancer of a tumor type, the method comprising the steps of:

a) extracting extracellular DNA from blood plasma or serum obtained from a human or animal, wherein the extracted extracellular DNA comprises DNA species from a plurality of the human's or animal's genes, wherein at least one of said DNA species is a non-mutated tumor-associated DNA species;

b) amplifying or signal amplifying DNA from two or more genes from a portion of the extracted extracellular DNA, wherein said genes are associated with neoplastic tissue, wherein at least one of said genes is a non-mutated tumor-associated gene and wherein the extracted extracellular DNA is amplified qualitatively or quantitatively, sequentially or concurrently, to produce an

amplified DNA fragment or amplified signal from each of the two or more genes comprising the portion of extracellular extracted DNA; and

c) detecting the amplified DNA fragments or amplified signals from said two or more genes, wherein detection of the genes identifies a propensity in the human or animal to have or develop a cancer.

17. (Currently amended) The method of claim 16, wherein the amplified DNA in part (b) comprises at least one non-mutated, wild-type DNA species.

18. (Original) The method of claim 16, wherein the genes amplified or signal amplified in step (b) are genes specific for cancer of a specific tumor type.

19. (Original) The method of claim 16, further comprising the step of assessing a human or animal for having cancer of a particular tumor type, wherein said specific cancer tumor type is colorectal cancer, lung cancer, breast cancer, lymphoma, pancreatic cancer, bladder cancer, ovarian cancer, esophageal cancer, hepatocellular cancer, cervical cancer, melanoma, sarcoma, or leukemia, and wherein the human or animal is determined to have a cancer of a particular tumor type when amplified DNA fragments or amplified signals of genes specific for cancer of said tumor type are detected.

20. (Original) The method of claim 19, whereby detection of said amplified DNA fragments or amplified signals demonstrates recurrence of a cancer tumor type.

21. (Original) The method of claim 16, wherein a least one DNA species associated with cancer is mutated, translocated, or otherwise altered.

22. (Original) The method of claim 1, 5, 10, or 16, wherein amplification in subpart (b) is performed using an amplification method that is polymerase chain reaction, ligase chain reaction, DNA signal amplification, boomerang DNA amplification, Q-beta replication,

transcription-based amplification, isothermal nucleic acid sequence based amplification, self-sustained sequence replication assay, strand displacement activation, cycling probe technology, or combinations or variations thereof.

23. (Original) The method of claim 1, 5, 10, or 16, wherein detection in subpart (c) is performed using a qualitative or quantitative detection method that is gel electrophoresis, immunological based detection, nucleic acid hybridization based detection, Southern blot analysis, electrochemiluminescence, reverse dot blot hybridization, high performance liquid chromatography, or combinations or variations thereof.

24. (Currently amended) A method of identifying a human or animal with a neoplastic disease, the method comprising the steps of:

a) extracting extracellular DNA from blood plasma or serum obtained from a human or animal, wherein the extracted extracellular DNA comprises DNA species from a plurality of the human's or animal's genes, wherein at least one of said DNA species is a non-mutated tumor-associated DNA species;

b) amplifying or signal amplifying DNA from two or more genes from a portion of the extracted extracellular DNA, wherein said genes are associated with neoplastic disease, wherein at least one of said genes is a non-mutated tumor-associated gene and wherein the extracted extracellular DNA is amplified qualitatively or quantitatively, sequentially or concurrently, to produce an amplified DNA fragment or amplified signal from each of the two or more genes comprising the portion of extracellular extracted DNA; and

c) amplified DNA fragments or amplified signals from said two or more genes, wherein detection of the genes identifies the human or animal as having a neoplastic disease.

25. (Original) The method of claim 24, wherein the neoplastic disease is cancer.

26. (Original) The method of claim 24, wherein the neoplastic disease is a premalignancy.

27. (Original) The method of claim 24, comprising the further step of selecting the human or animal for additional diagnostic testing.

28. (Original) The method of claim 24, comprising the further step of selecting the human or animal for a therapy.

29. (Original) The method of claim 1, wherein one DNA associated with cancer is K-ras DNA, c-myc DNA, p16 DNA, her-2/neu DNA, src DNA, fos DNA, jun DNA, bcl-2 DNA, bcl-2/Igh DNA, Von Hippel-Lindau gene DNA, p53 DNA, retinoblastoma gene DNA, mutated in colon cancer gene DNA, adenomatous polyposis coli gene DNA, deleted in colon cancer gene DNA, epidermal growth factor receptor DNA, or epidermal growth factor DNA.

30. (Original) The method of claim 5, wherein one DNA associated with cancer is K-ras DNA, c-myc DNA, p16 DNA, her-2/neu DNA, src DNA, fos DNA, jun DNA, bcl-2 DNA, bcl-2/Igh DNA, Von Hippel-Lindau gene DNA, p53 DNA, retinoblastoma gene DNA, mutated in colon cancer gene DNA, adenomatous polyposis coli gene DNA, deleted in colon cancer gene DNA, epidermal growth factor receptor DNA, or epidermal growth factor DNA.

31. (Original) The method of claim 10, wherein one DNA associated with neoplastic tissue is K-ras DNA, c-myc DNA, p16 DNA, her-2/neu DNA, src DNA, fos DNA, jun DNA, bcl-2 DNA, bcl-2/Igh DNA, Von Hippel-Lindau gene DNA, p53 DNA, retinoblastoma gene DNA, mutated in colon cancer gene DNA, adenomatous polyposis coli gene DNA, deleted in colon cancer gene DNA, epidermal growth factor receptor DNA, or epidermal growth factor DNA.

33. (Original) The method of claim 16, wherein one DNA associated with cancer is K-ras DNA, c-myc DNA, p16 DNA, her-2/neu DNA, src DNA, fos DNA, jun DNA, bcl-2 DNA, bcl-2/Igh DNA, Von Hippel-Lindau gene DNA, p53 DNA, retinoblastoma gene DNA, mutated in colon cancer gene DNA, adenomatous polyposis coli gene DNA, deleted in colon cancer gene DNA, epidermal growth factor receptor DNA, or epidermal growth factor DNA.

34. (Previously presented) The method of claim 25, wherein one DNA associated with neoplastic disease is K-ras DNA, c-myc DNA, p16 DNA, her-2/neu DNA, src DNA, fos DNA, jun DNA, bcl-2 DNA, bcl-2/Igh DNA, Von Hippel-Lindau gene DNA, p53 DNA, retinoblastoma gene DNA, mutated in colon cancer gene DNA, adenomatous polyposis coli gene DNA, deleted in colon cancer gene DNA, epidermal growth factor receptor DNA, or epidermal growth factor DNA.